# 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt SEQUENCE LISTING

<110> Monsanto Technology LLC

Baum, James A. Donovan, Judith C.

Donovan, William P.

Engleman, James T.

Krasomil-Osterfeld, Karina

Pitkin, John W.

Roberts, James K.

- <120> Insecticidal Proteins Secreted From Bacillus Species and Uses Therefor
- <130> 38-21(52806)PCT
- <150> US 60/485,483
- <151> 2003-07-07
- <160> 33
- <170> PatentIn version 3.1
- <210> 1
- <211> 15
- <212> PRT
- <213> Bacillus thuringiensis
- <400> 1
- <210> 2
- <211> 45

|                  |                  |                  |                  |                  | 3 ℧ ─ Ͻ・         | 1(ちつ)            | ないとい             | Sag              | HONC             | 011              | ctin             | ~ DC             | т э              |                  |                  |     |
|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| <212             | > [              | NA               |                  | ,                | JU-2.            | 1(32             | 000)             | зец              | uenc             | C L.I            | 3 L I I I        | y_PC             | 1_2.             | 5125             | .txt             |     |
| <213             | > A              | rtif             | icia             | 1 Se             | quen             | ce               |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
|                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <220             | >                |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <223             | > t              | ic g             | ene              | prob             | e en             | codi             | ng S             | EQ I             | D NO             | 1                |                  |                  |                  |                  |                  |     |
| <400<br>gtaa     |                  | gac c            | atat             | gcag             | a at             | cata             | tatt             | gat              | acga             | gta              | caag             | ıa               |                  |                  |                  | 45  |
| <210             | > 3              | 3                |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <211             | > 1              | L253             |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <212             | > [              | DNA              |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <213             | > E              | Bacil            | lus              | thur             | ingi             | ensi             | s                |                  |                  |                  |                  |                  |                  |                  |                  |     |
|                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <220             | -                |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <221             |                  | CDS              |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <222             |                  | (153)            | (1               | .253)            | 1                |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <223             | <b>&gt;</b>      |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| -400             |                  | ,                |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |     |
| <400<br>aatt     |                  | 3<br>att t       | taat             | atto             | t ta             | itgti            | atto             | cta              | ataat            | ata              | caat             | aaaa             | agc a            | ataat            | tatcc            | 60  |
| ttca             | tat              | tat g            | jttta            | ıtaaa            | at tt            | aata             | aaat             | aca              | ataaa            | aaat             | agag             | gtgtt            | at a             | aatat            | ttttg            | 120 |
| aaag             | jcgt:            | tat d            | aaga             | ıgtga            | at gg            | gaggg            | gataa            | tt               | atg<br>Met<br>1  | aaa<br>Lys       | aat<br>Asn       | aga<br>Arg       | ttt<br>Phe<br>5  | tca<br>Ser       | aaa<br>Lys       | 173 |
| gtg<br>Val       | gca<br>Ala       | tta<br>Leu<br>10 | tgc<br>Cys       | acc<br>Thr       | gta<br>Val       | ccg<br>Pro       | att<br>Ile<br>15 | tta<br>Leu       | atg<br>Met       | gtt<br>Val       | tct<br>Ser       | aca<br>Thr<br>20 | ttc<br>Phe       | gcc<br>Ala       | agt<br>Ser       | 221 |
| tca<br>Ser       | agc<br>Ser<br>25 | atg<br>Met       | tca<br>Ser       | gct<br>Ala       | ttt<br>Phe       | gct<br>Ala<br>30 | gca<br>Ala       | gaa<br>Glu       | gcc<br>Ala       | aaa<br>Lys       | tca<br>Ser<br>35 | cca<br>Pro       | gat<br>Asp       | tta<br>Leu       | aat<br>Asn       | 269 |
| gta<br>Val<br>40 | tct<br>Ser       | caa<br>Gln       | caa<br>Gln       | gta<br>Val       | ata<br>Ile<br>45 | ggt<br>Gly       | ccc<br>Pro       | tat<br>Tyr       | gcc<br>Ala       | gaa<br>Glu<br>50 | tct<br>Ser       | tat<br>Tyr       | att<br>Ile       | gat<br>Asp       | att<br>Ile<br>55 | 317 |
| gtg<br>Val       | cag<br>Gln       | gat<br>Asp       | aga<br>Arg       | atg<br>Met<br>60 | aaa<br>Lys       | caa<br>Gln       | agg<br>Arg       | gat<br>Asp       | aag<br>Lys<br>65 | gga<br>Gly       | tca<br>Ser       | aaa<br>Lys       | tta<br>Leu       | act<br>Thr<br>70 | ggt<br>Gly       | 365 |
| aaa<br>Lys       | cca<br>Pro       | ata<br>Ile       | aat<br>Asn<br>75 | atg<br>Met       | caa<br>Gln       | gaa<br>Glu       | caa<br>Gln       | ata<br>Ile<br>80 | ata<br>Ile       | gat<br>Asp       | ggg<br>Gly       | tgg<br>Trp       | ttt<br>Phe<br>85 | cta<br>Leu       | gct<br>Ala       | 413 |

| aga<br>Arg        | ttt<br>Phe        | tgg<br>Trp<br>90  | ata<br>Ile        | ttt               | 38-2<br>aag<br>Lys | gat               | caa               | aac               | aat               | aac               | cat               | cag               | aca               | aat               | .txt<br>aga<br>Arg | 461  |
|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|------|
| ttt<br>Phe        | ata<br>Ile<br>105 | tcc<br>Ser        | tgg<br>Trp        | ttt<br>Phe        | aaa<br>Lys         | gat<br>Asp<br>110 | aat<br>Asn        | att<br>Ile        | gct<br>Ala        | agt<br>Ser        | tca<br>Ser<br>115 | aaa<br>Lys        | ggg<br>Gly        | tat<br>Tyr        | aat<br>Asn         | 509  |
| agt<br>Ser<br>120 | att<br>Ile        | gcg<br>Ala        | gag<br>Glu        | caa<br>Gln        | atg<br>Met<br>125  | ggt<br>Gly        | tta<br>Leu        | aaa<br>Lys        | ata<br>Ile        | gaa<br>Glu<br>130 | gca<br>Ala        | gaa<br>Glu        | aac<br>Asn        | gat<br>Asp        | atg<br>Met<br>135  | 557  |
| gat<br>Asp        | gta<br>Val        | aca<br>Thr        | aat<br>Asn        | ata<br>Ile<br>140 | gat<br>Asp         | tat<br>Tyr        | aca<br>Thr        | tct<br>Ser        | aag<br>Lys<br>145 | aca<br>Thr        | ggc<br>Gly        | gat<br>Asp        | acc<br>Thr        | att<br>Ile<br>150 | tat<br>Tyr         | 605  |
| aat<br>Asn        | ggt<br>Gly        | att<br>Ile        | tca<br>Ser<br>155 | gaa<br>Glu        | ttg<br>Leu         | aaa<br>Lys        | aat<br>Asn        | tat<br>Tyr<br>160 | aca<br>Thr        | gga<br>Gly        | tca<br>Ser        | act<br>Thr        | caa<br>Gln<br>165 | aag<br>Lys        | atg<br>Met         | 653  |
| aaa<br>Lys        | aca<br>Thr        | gat<br>Asp<br>170 | agt<br>Ser        | ttt<br>Phe        | caa<br>Gln         | aga<br>Arg        | gat<br>Asp<br>175 | tat<br>Tyr        | aca<br>Thr        | aaa<br>Lys        | tca<br>Ser        | gaa<br>Glu<br>180 | tct<br>Ser        | act<br>Thr        | tca<br>Ser         | 701  |
| gta<br>Val        | act<br>Thr<br>185 | aat<br>Asn        | gga<br>Gly        | tta<br>Leu        | caa<br>Gln         | tta<br>Leu<br>190 | gga<br>Gly        | ttt<br>Phe        | aaa<br>Lys        | gtt<br>Val        | gct<br>Ala<br>195 | gct<br>Ala        | aaa<br>Lys        | gga<br>Gly        | gta<br>Val         | 749  |
| gtt<br>Val<br>200 | gct<br>Ala        | ttg<br>Leu        | gct<br>Ala        | ggg<br>Gly        | gca<br>Ala<br>205  | gac<br>Asp        | ttt<br>Phe        | gaa<br>Glu        | acc<br>Thr        | agt<br>Ser<br>210 | gtt<br>Val        | act<br>Thr        | tat<br>Tyr        | aat<br>Asn        | cta<br>Leu<br>215  | 797  |
| tca<br>Ser        | act<br>Thr        | act<br>Thr        | aca<br>Thr        | act<br>Thr<br>220 | gaa<br>Glu         | aca<br>Thr        | aat<br>Asn        | aca<br>Thr        | ata<br>Ile<br>225 | tca<br>Ser        | gac<br>Asp        | aag<br>Lys        | ttt<br>Phe        | act<br>Thr<br>230 | gtc<br>Val         | 845  |
| cca<br>Pro        | tct<br>Ser        | caa<br>Gln        | gaa<br>Glu<br>235 | gtt<br>Val        | aca<br>Thr         | ttg<br>Leu        | cct<br>Pro        | cca<br>Pro<br>240 | gga<br>Gly        | cat<br>His        | aaa<br>Lys        | gcg<br>Ala        | ata<br>Ile<br>245 | gtg<br>Val        | aaa<br>Lys         | 893  |
| cat<br>His        | gat<br>Asp        | tta<br>Leu<br>250 | aga<br>Arg        | aaa<br>Lys        | atg<br>Met         | gtt<br>Val        | tat<br>Tyr<br>255 | tct<br>Ser        | ggt<br>Gly        | act<br>Thr        | cat<br>His        | gat<br>Asp<br>260 | cta<br>Leu        | aag<br>Lys        | ggt<br>Gly         | 941  |
| gat<br>Asp        | tta<br>Leu<br>265 | Tie               | gtg<br>Val        | agt<br>Ser        | ttt<br>Phe         | aat<br>Asn<br>270 | gat<br>Asp        | aaa<br>Lys        | gag<br>Glu        | att<br>Ile        | gta<br>Val<br>275 | caa<br>Gln        | aaa<br>Lys        | ttt<br>Phe        | att<br>Ile         | 989  |
| tat<br>Tyr<br>280 | cca<br>Pro        | aat<br>Asn        | tat<br>Tyr        | aga<br>Arg        | gaa<br>Glu<br>285  | att<br>Ile        | aat<br>Asn        | tta<br>Leu        | tct<br>Ser        | gat<br>Asp<br>290 | atc<br>Ile        | cgt<br>Arg        | gaa<br>Glu        | act<br>Thr        | atg<br>Met<br>295  | 1037 |
| att<br>Ile        | gaa<br>Glu        | att<br>Ile        | gat<br>Asp        | gaa<br>Glu<br>300 | tgg<br>Trp         | aat<br>Asn        | cat<br>His        | gta<br>Val        | aac<br>Asn<br>305 | cct<br>Pro        | gtg<br>Val        | aat<br>Asn        | ttt<br>Phe        | tat<br>Tyr<br>310 | gaa<br>Glu         | 1085 |
| tta<br>Leu        | gtt<br>Val        | ggg<br>Gly        | gtc<br>Val<br>315 | aaa<br>Lys        | aat<br>Asn         | cat<br>His        | ata<br>Ile        | aaa<br>Lys<br>320 | aat<br>Asn        | ggt<br>Gly        | gaa<br>Glu        | act<br>Thr        | ttg<br>Leu<br>325 | tat<br>Tyr        | ata<br>Ile         | 1133 |
| gat<br>Asp        | act<br>Thr        | cca<br>Pro<br>330 | Ala               | aaa<br>Lys        | ttt<br>Phe         | atg<br>Met        | ttt<br>Phe<br>335 | aat<br>Asn        | ggt<br>Gly        | gct<br>Ala        | aat<br>Asn        | cca<br>Pro<br>340 | tat<br>Tyr        | tat<br>Tyr        | aga<br>Arg         | 1181 |

Page 3

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

gca aca ttt aca gaa tac gac ggg aat aat cct gtt caa aca aag 1229 Ala Thr Phe Thr Glu Tyr Asp Gly Asn Asn Pro Val Gln Thr Lys 345 350

gta tta agt gaa aac ttt aaa ttg Val Leu Ser Glu Asn Phe Lys Leu 360 365

1253

<210> 4

<211> 367

<212> PRT

<213> Bacillus thuringiensis

<400> 4

Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu 1 5 10 15

Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu 20 25 30

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp 50 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile 100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys 115 120 125

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Page 4

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt 165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr 210 225 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro 225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys 260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Glu Ile Asn Leu 275 280 285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val 290 295 300

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys 305 310 315

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn 325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn 340 345 350

Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu 355 360 365

<210> 5

<211> 1621

<212> DNA

<213> Bacillus thuringiensis

<220>

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<221> CDS

<222> (530)..(1621)

<223>

<400> actagttttt tcataatggc ataagcggga tgatgatctt gttttttacg atgttcaata 60 tccaatgtgt gcctttctat atcaatcgca cgatataaat aacactattt ccctttgaat 120 tttatatagg tttcatctaa ttttcaagac atgtggttgt tttgcgtttt cttcttccaa 180 atttgataaa tcaagctccc atattcatga atccagcgca taatgattgt gggatgaact 240 gaaacatcac gatagcttaa agcaaaacga caatagtagc ggacggctac cataataata 300 tcttgtttga actgtttccc tttaaaatat cacatttgtg attctcctcg atgcttttt 360 tagagtgtag cttcatctag aacactttgc aatagaacca ttcctttgat atacaattaa 420 accacattta tccttcatgg aatgtttata tattaaagaa tataaaaaaa catacgatgt 480 tataattaat ttgaaagcgt taacaaaaat gaatgatgga gggataatt atg aaa tac 538 Met Lys Tyr aag ttt tca aaa gtc gtt aag tgt act tta cca gct tta atg att act Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu Met Ile Thr 5 10 15586 aca ttc gtt act cca agt atg gca gtt ttt gcc gca gaa acc aag tcg Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu Thr Lys Ser 20 25 30 634 cca aat cta aat gca tct caa caa gca ata act cca tat gct gaa tct Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr Ala Glu Ser 682 tat att gat act gtt caa gat aga atg aaa caa aga gat agg gaa tca Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp Arg Glu Ser 730 aaa cta act ggt aaa cca ata aat atg caa gaa caa ata ata gat gga 778 Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly tgg ttt tta gct aga ttc tgg ata ttt aaa gat caa aat aac aat cat Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His 826 90 95 caa aca aat aga ttt ata tcc tgg ttt aaa gat aat ctt gct agt tcg Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Ser 874 aag ggg tat gac agt ata gca gaa caa atg ggc tta aaa ata gaa gca Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala 922 120 tta aat gat atg gat gta aca aat att gat tat aca tct aaa aca ggt Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly 970

Page 6

|                   |                   |                   | 135               |                   | 38-2              | 21(52             | 2806)             | ) Sec<br>140      | quen       | ce L              | isti              | ng_P              | CT_2<br>145       | .ST2       | 5.txt             |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|------|
| gat<br>Asp        | acc<br>Thr        | ata<br>Ile<br>150 | ı yı              | aat<br>Asn        | gga<br>Gly        | att<br>Ile        | tct<br>Ser<br>155 | gaa<br>Glu        | cta<br>Leu | aca<br>Thr        | aat<br>Asn        | tat<br>Tyr<br>160 | aca<br>Thr        | gga<br>Gly | aca<br>Thr        | 1018 |
| acc<br>Thr        | caa<br>Gln<br>165 | aaa<br>Lys        | atg<br>Met        | aaa<br>Lys        | acc<br>Thr        | gat<br>Asp<br>170 | agt<br>Ser        | ttt<br>Phe        | caa<br>Gln | aga<br>Arg        | gat<br>Asp<br>175 | tat<br>Tyr        | aca<br>Thr        | aaa<br>Lys | tct<br>Ser        | 1066 |
| gaa<br>Glu<br>180 |                   | act<br>Thr        | tca<br>Ser        | gta<br>Val        | aca<br>Thr<br>185 | aat<br>Asn        | ggg<br>Gly        | tta<br>Leu        | caa<br>Gln | tta<br>Leu<br>190 | gga<br>Gly        | ttt<br>Phe        | aaa<br>Lys        | gtt<br>Val | gct<br>Ala<br>195 | 1114 |
|                   | _,,,              | Giy               | Vai               | 200               | Ala               | Leu               | Ala               | ggt<br>Gly        | 205        | ASP               | Phe               | Glu               | Thr               | Ser<br>210 | Val               | 1162 |
| acc<br>Thr        | tat<br>Tyr        | aat<br>Asn        | tta<br>Leu<br>215 | tca<br>Ser        | tct<br>Ser        | act<br>Thr        | aca<br>Thr        | act<br>Thr<br>220 | gaa<br>Glu | aca<br>Thr        | aat<br>Asn        | aca<br>Thr        | ata<br>Ile<br>225 | tcg<br>Ser | gat<br>Asp        | 1210 |
| _, _              |                   | 230               | vai               | F1 0              | 261               | GIII              | 235               | gtt<br>Val        | ınr        | Leu               | Ser               | Pro<br>240        | Gly               | His        | Lys               | 1258 |
| gca<br>Ala        | gtg<br>Val<br>245 | gtg<br>Val        | aaa<br>Lys        | cat<br>His        | gat<br>Asp        | ttg<br>Leu<br>250 | aga<br>Arg        | aaa<br>Lys        | atg<br>Met | gtg<br>Val        | tat<br>Tyr<br>255 | ttt<br>Phe        | ggg<br>Gly        | act<br>Thr | cat<br>His        | 1306 |
| gat<br>Asp<br>260 | tta<br>Leu        | aag<br>Lys        | ggt<br>Gly        | gat<br>Asp        | tta<br>Leu<br>265 | aaa<br>Lys        | gta<br>Val        | ggt<br>Gly        | ttt<br>Phe | aat<br>Asn<br>270 | gat<br>Asp        | aaa<br>Lys        | gag<br>Glu        | att<br>Ile | gta<br>Val<br>275 | 1354 |
|                   | _,,               |                   |                   | 280               | 710               | ASII              | ıyı               | aga<br>Arg        | 285        | TIE               | ASP               | Leu               | Ser               | Asp<br>290 | Ile               | 1402 |
| cgt<br>Arg        | aaa<br>Lys        | aca<br>Thr        | atg<br>Met<br>295 | att<br>Ile        | gaa<br>Glu        | att<br>Ile        | gat<br>Asp        | aaa<br>Lys<br>300 | tgg<br>Trp | aat<br>Asn        | cat<br>His        | gta<br>Val        | aat<br>Asn<br>305 | acc<br>Thr | att<br>Ile        | 1450 |
| gac<br>Asp        | ttt<br>Phe        | tat<br>Tyr<br>310 | caa<br>Gln        | tta<br>Leu        | gtt<br>Val        | gga<br>Gly        | gtt<br>Val<br>315 | aaa<br>Lys        | aat<br>Asn | cat<br>His        | ata<br>Ile        | aaa<br>Lys<br>320 | aat<br>Asn        | ggt<br>Gly | gat<br>Asp        | 1498 |
| act<br>Thr        | tta<br>Leu<br>325 | tat<br>Tyr        | ata<br>Ile        | gat<br>Asp        | acc<br>Thr        | ccg<br>Pro<br>330 | gcc<br>Ala        | gaa<br>Glu        | ttt<br>Phe | aca<br>Thr        | ttt<br>Phe<br>335 | aat<br>Asn        | gga<br>Gly        | gct<br>Ala | aat<br>Asn        | 1546 |
| cca<br>Pro<br>340 | tat<br>Tyr        | tat<br>Tyr        | aga<br>Arg        | gca<br>Ala        | aca<br>Thr<br>345 | ttt<br>Phe        | aca<br>Thr        | gaa<br>Glu        | tac<br>Tyr | gac<br>Asp<br>350 | gag<br>Glu        | aac<br>Asn        | gga<br>Gly        | aat<br>Asn | cct<br>Pro<br>355 | 1594 |
| gtt<br>Val        | caa<br>Gln        | aca<br>Thr        | aag<br>Lys        | att<br>Ile<br>360 | tta<br>Leu        | agt<br>Ser        | gga<br>Gly        | aat<br>Asn        |            |                   |                   |                   |                   |            |                   | 1621 |

<210> 6

<211> 364

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<212> PRT

<213> Bacillus thuringiensis

<400> 6

Met Lys Tyr Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu 1 5 10 15

Met Ile Thr Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu 20 25 30

Thr Lys Ser Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr 35 40 45

Ala Glu Ser Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp 50 55 60

Arg Glu Ser Lys Leu Thr Gly Lys Pro Ile Asm Met Gln Glu Gln Ile 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu 100 105 110

Ala Ser Ser Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys 115 120 125

Ile Glu Ala Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr 145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr 165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr Glu Thr Asn Thr 210 220

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro 225 230 235 240 Gly His Lys Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe 245 250 255 Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys 260 265 270 Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu 275 280 285 Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val 290 295 300 Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys 305 310 315 320 Asn Gly Asp Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn 325 330 335 Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Glu Asn 340 345 350 Gly Asn Pro Val Gln Thr Lys Ile Leu Ser Gly Asn 355 <210> <211> 1552 <212> DNA Bacillus thuringiensis <213> <220> <221> **CDS** <222> (169)..(1272)<223> <400> ctagctgaat atgcagtaga taatgatttt gactatacta atgagatttt ttatgtaata

c400> /
ctagctgaat atgcagtaga taatgatttt gactatacta atgagatttt ttatgtaata 60
aaccatattt atccttaaat aaatgttcac atatttaaaa agaataaact accatgcggt 120
gctagaatat aaatgagagc gctaacaaaa aataatggag ggataatc atg aaa tac 177
Page 9

|                   |                   |                   |                   |                   | 38-2              | 1(52              | 806)              | Seq               | uenc              | e Li              | stin              | g_PC              |                   |                   | .txt<br>Tyr       |   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---|-----|
| aaa<br>Lys        | tca<br>Ser<br>5   | tca<br>Ser        | aaa<br>Lys        | gta<br>Val        | gca<br>Ala        | ata<br>Ile<br>10  | tgt<br>Cys        | act<br>Thr        | tta<br>Leu        | tca<br>Ser        | gct<br>Ala<br>15  | tta<br>Leu        | atg<br>Met        | ctt<br>Leu        | tca<br>Ser        | ; | 225 |
| aca<br>Thr<br>20  | att<br>Ile        | ggt<br>Gly        | act<br>Thr        | tcg<br>Ser        | agt<br>Ser<br>25  | atg<br>Met        | tcc<br>Ser        | act<br>Thr        | ttt<br>Phe        | gct<br>Ala<br>30  | gca<br>Ala        | gaa<br>Glu        | aca<br>Thr        | aca<br>Thr        | tta<br>Leu<br>35  | : | 273 |
| cca<br>Pro        | ggt<br>Gly        | caa<br>Gln        | act<br>Thr        | ctt<br>Leu<br>40  | aag<br>Lys        | gaa<br>Glu        | caa<br>Gln        | tca<br>Ser        | ata<br>Ile<br>45  | acc<br>Thr        | cca<br>Pro        | cgt<br>Arg        | gca<br>Ala        | gaa<br>Glu<br>50  | tct<br>Ser        | - | 321 |
| tat<br>Tyr        | att<br>Ile        | gat<br>Asp        | att<br>Ile<br>55  | gta<br>Val        | caa<br>Gln        | gat<br>Asp        | aga<br>Arg        | atg<br>Met<br>60  | aaa<br>Lys        | caa<br>Gln        | agg<br>Arg        | gat<br>Asp        | ata<br>Ile<br>65  | gaa<br>Glu        | tcg<br>Ser        |   | 369 |
| aaa<br>Lys        | cgt<br>Arg        | act<br>Thr<br>70  | ggt<br>Gly        | aaa<br>Lys        | ccg<br>Pro        | att<br>Ile        | aat<br>Asn<br>75  | atg<br>Met        | caa<br>Gln        | gaa<br>Glu        | caa<br>Gln        | ata<br>Ile<br>80  | ata<br>Ile        | gat<br>Asp        | gga<br>Gly        |   | 417 |
| tgg<br>Trp        | ttt<br>Phe<br>85  | tta<br>Leu        | gca<br>Ala        | aga<br>Arg        | ttc<br>Phe        | tgg<br>Trp<br>90  | ata<br>Ile        | ttt<br>Phe        | aaa<br>Lys        | gat<br>Asp        | caa<br>Gln<br>95  | aat<br>Asn        | aat<br>Asn        | aac<br>Asn        | cat<br>His        |   | 465 |
| caa<br>Gln<br>100 | aca<br>Thr        | aat<br>Asn        | aga<br>Arg        | ttc<br>Phe        | ata<br>Ile<br>105 | aca<br>Thr        | tgg<br>Trp        | ttt<br>Phe        | aaa<br>Lys        | aat<br>Asn<br>110 | aat<br>Asn        | gtt<br>Val        | gcc<br>Ala        | agc<br>Ser        | tca<br>Ser<br>115 |   | 513 |
| aaa<br>Lys        | ggt<br>Gly        | tat<br>Tyr        | gag<br>Glu        | ggt<br>Gly<br>120 | att<br>Ile        | gca<br>Ala        | gaa<br>Glu        | caa<br>Gln        | atg<br>Met<br>125 | ggt<br>Gly        | ttg<br>Leu        | aaa<br>Lys        | ata<br>Ile        | gaa<br>Glu<br>130 | tcg<br>Ser        |   | 561 |
| atg<br>Met        | agt<br>Ser        | gat<br>Asp        | atg<br>Met<br>135 | aat<br>Asn        | gta<br>Val        | tcg<br>Ser        | aat<br>Asn        | ata<br>Ile<br>140 | aat<br>Asn        | tat<br>Tyr        | aca<br>Thr        | ggt<br>Gly        | aaa<br>Lys<br>145 | aag<br>Lys        | ggt<br>Gly        |   | 609 |
| gat<br>Asp        | act<br>Thr        | ata<br>Ile<br>150 | tat<br>Tyr        | aat<br>Asn        | ggc<br>Gly        | gtt<br>Val        | tcg<br>Ser<br>155 | gaa<br>Glu        | tta<br>Leu        | gaa<br>Glu        | aat<br>Asn        | aaa<br>Lys<br>160 | atg<br>Met        | gga<br>Gly        | aca<br>Thr        |   | 657 |
| cct<br>Pro        | caa<br>Gln<br>165 | aaa<br>Lys        | atg<br>Met        | aaa<br>Lys        | tca<br>Ser        | gat<br>Asp<br>170 | agt<br>Ser        | ttt<br>Phe        | caa<br>Gln        | aga<br>Arg        | gat<br>Asp<br>175 | tat<br>Tyr        | acc<br>Thr        | aaa<br>Lys        | tct<br>Ser        |   | 705 |
| caa<br>Gln<br>180 | Ser               | acc<br>Thr        | tca<br>Ser        | gta<br>Val        | aca<br>Thr<br>185 | Asn               | ggg<br>Gly        | tta<br>Leu        | caa<br>Gln        | tta<br>Leu<br>190 | gga<br>Gly        | gtt<br>Val        | aaa<br>Lys        | gtt<br>Val        | tct<br>Ser<br>195 |   | 753 |
| gcc<br>Ala        | aaa<br>Lys        | ggt<br>Gly        | acg<br>Thr        | gtt<br>Val<br>200 | Va I              | tta<br>Leu        | gga<br>Gly        | gag<br>Glu        | gca<br>Ala<br>205 | Ser               | ctt<br>Leu        | gaa<br>Glu        | aca<br>Thr        | agc<br>Ser<br>210 | ٧a٦               |   | 801 |
| act<br>Thr        | tat<br>Tyr        | aat<br>Asn        | tta<br>Leu<br>215 | Ser               | tct<br>Ser        | act<br>Thr        | gca<br>Ala        | act<br>Thr<br>220 | Glu               | aca<br>Thr        | gat<br>Asp        | aca<br>Thr        | aca<br>Thr<br>225 | Ser               | gac<br>Asp        |   | 849 |
| aag<br>Lys        | ttt<br>Phe        | act<br>Thr<br>230 | ٧a٦               | cca<br>Pro        | tcc<br>ser        | caa<br>Gln        | gaa<br>Glu<br>235 | gtt<br>Val        | aca<br>Thr        | tta<br>Leu        | cca<br>Pro        | cca<br>Pro<br>240 | ĞÎy               | cat<br>His        | aaa<br>Lys        |   | 897 |

|                   |                   |                   |                   |                   | 38-2              | 1(52              | 806)              | Sea               | uenc              | e Li              | stin              | a PC              | т 2.              | ST25              | .txt              |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| gca<br>Ala        | gta<br>Val<br>245 | att<br>Ile        | aag<br>Lys        | cat<br>His        | gat               | tta               | aga               | aaa               | atg               | gtg               | tat               | tct               | aat               | acg<br>Thr        | cat               | 945  |
| gac<br>Asp<br>260 | tta<br>Leu        | aag<br>Lys        | ggg<br>Gly        | gat<br>Asp        | tta<br>Leu<br>265 | aaa<br>Lys        | gta<br>Val        | gct<br>Ala        | ttt<br>Phe        | aac<br>Asn<br>270 | gat<br>Asp        | aaa<br>Lys        | gca<br>Ala        | att<br>Ile        | gta<br>Val<br>275 | 993  |
| caa<br>Gln        | aaa<br>Lys        | ttt<br>Phe        | att<br>Ile        | tat<br>Tyr<br>280 | cca<br>Pro        | aat<br>Asn        | tat<br>Tyr        | aga<br>Arg        | tct<br>Ser<br>285 | ata<br>Ile        | aat<br>Asn        | tta<br>Leu        | tct<br>Ser        | gat<br>Asp<br>290 | att<br>Ile        | 1041 |
| cgt<br>Arg        | aaa<br>Lys        | aca<br>Thr        | atg<br>Met<br>295 | aaa<br>Lys        | gaa<br>Glu        | att<br>Ile        | gat<br>Asp        | gaa<br>Glu<br>300 | tgg<br>Trp        | aat<br>Asn        | cat<br>His        | gta<br>Val        | aaa<br>Lys<br>305 | ccc<br>Pro        | att<br>Ile        | 1089 |
| gat<br>Asp        | ttt<br>Phe        | tat<br>Tyr<br>310 | caa<br>Gln        | ctg<br>Leu        | gtt<br>Val        | gga<br>Gly        | ata<br>Ile<br>315 | aaa<br>Lys        | aat<br>Asn        | cat<br>His        | ata<br>Ile        | aaa<br>Lys<br>320 | aat<br>Asn        | ggg<br>Gly        | gat<br>Asp        | 1137 |
| acc<br>Thr        | tta<br>Leu<br>325 | tat<br>Tyr        | ata<br>Ile        | gag<br>Glu        | act<br>Thr        | cca<br>Pro<br>330 | gct<br>Ala        | aaa<br>Lys        | ttt<br>Phe        | att<br>Ile        | ttt<br>Phe<br>335 | aat<br>Asn        | gga<br>Gly        | gct<br>Ala        | aat<br>Asn        | 1185 |
| gta<br>Val<br>340 | ıyr               | tat<br>Tyr        | aga<br>Arg        | gca<br>Ala        | act<br>Thr<br>345 | ttt<br>Phe        | aca<br>Thr        | gaa<br>Glu        | tat<br>Tyr        | gat<br>Asp<br>350 | aag<br>Lys        | gat<br>Asp        | gga<br>Gly        | aaa<br>Lys        | cct<br>Pro<br>355 | 1233 |
| gtt<br>Val        | caa<br>Gln        | ttc<br>Phe        | aac<br>Asn        | aaa<br>Lys<br>360 | ttt<br>Phe        | tta<br>Leu        | agt<br>Ser        | gaa<br>Glu        | aat<br>Asn<br>365 | tac<br>Tyr        | aag<br>Lys        | tta<br>Leu        | tag               | agga              | agt               | 1282 |
| aaa               | gatg              | ccg ·             | tagt              | gaga <sup>.</sup> | tc g              | tttc              | acag              | c ta              | ctga              | gtat              | tcaa              | aata              | ata               | cacg              | ggaaaa            | 1342 |
| ttc               | acct <sup>.</sup> | tcc               | tgga              | agga              | cg g              | attt              | actt              | t tt              | ttac              | ggag              | gaa               | cttg              | ttt               | tata              | catcaa            | 1402 |
| aat               | gttt              | ttt               | tatg              | aggt              | tt g              | tgta <sup>.</sup> | ttct <sup>.</sup> | t at              | ttga              | gcct              | gga               | acgg              | aac               | catt              | ttgagt            | 1462 |
| aag               | ctta              | att               | tgac              | ttgg              | aa a              | tgta <sup>.</sup> | tttt              | t at              | tacc              | ttat              | tac               | gtga              | aca .             | atgg              | cctata            | 1522 |
| aac               | gtgc              | cac               | acag              | gaat              | gg g              | agga              | cgag <sup>.</sup> | t                 |                   |                   |                   |                   |                   |                   |                   | 1552 |

<210> 8

<211> 368

<212> PRT

<213> Bacillus thuringiensis

<400> 8

Met Lys Tyr Lys Ser Ser Lys Val Ala Ile Cys Thr Leu Ser Ala Leu 10 15

Met Leu Ser Thr Ile Gly Thr Ser Ser Met Ser Thr Phe Ala Ala Glu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt
Thr Thr Leu Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg
35 40 45 Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp 50 60 Ile Glu Ser Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile 65 70 75 80 Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn 85 90 95 Asn Asn His Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val 100 105 110 Ala Ser Ser Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys 115 120 125 Ile Glu Ser Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly
130
140 Lys Lys Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys 145 150 160 Met Gly Thr Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr 165 170 175 Thr Lys Ser Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val 180 185 190 Lys Val Ser Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu
195 200 205 Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr 210 220 Thr Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro 225 230 235 240 Gly His Lys Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr 245 250 255 Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys 260 265 270 Ala Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu 275 280 . 285

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt Ser Asp Ile Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val 290 295 300 Lys Pro Ile Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys 305 310 315 320 Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn 325 330 335 Gly Ala Asn Val Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Lys Asp 340 345 350 Gly Lys Pro Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu 355 360 365 <210> 9 <211> 1378 <212> DNA <213> Bacillus thuringiensis <220> <221> **CDS** (215)..(1306) <222> <223> <400> Cagtggatag gaatttgttt tcgtgctagg tatcaattta atttgttcta taagataagt 60 gaagtacgat caaaatgaat acttttgtgt attagatcaa taggtaaaat aataataaat 120 180 tttatatttg aaccttaaaa aattatttaa tcaaatcttt ttcactttaa aaacaaaata tccagaaaaa acaatagtta acggagggat aata atg aaa tac aag tca tca aaa Met Lys Tyr Lys Ser Ser Lys 1 5 235 gta gca atg tgt aca tta tca gct tta atg ctt tcg aca atc gcc act Val Ala Met Cys Thr Leu Ser Ala Leu Met Leu Ser Thr Ile Ala Thr 10 15 20283 cca agt ata tct gtt ttc gct gca gaa aca act tcg tca cat gcg gtt
Pro Ser Ile Ser Val Phe Ala Ala Glu Thr Thr Ser Ser His Ala Val
25 30 35 331 act aat cag caa aca att acg cag cgt gca gaa tct tat att gat att Thr Asn Gln Gln Thr Ile Thr Gln Arg Ala Glu Ser Tyr Ile Asp Ile 40 45 50 55379

|                           |                   |                   |                   | 38-2              | T(25              | 806)              | Seq               | uenc              | e Lı              | stin              | g_PC              | T_2.              | ST25              | .txt              |      |
|---------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| tg cac<br>al His          | aat<br>Asn        | aga<br>Arg        | atg<br>Met<br>60  | aaa<br>Lys        | caa<br>Gln        | aga<br>Arg        | gat<br>Asp        | att<br>Ile<br>65  | gaa<br>Glu        | tca<br>Ser        | aaa<br>Lys        | atg<br>Met        | aca<br>Thr<br>70  | ggt<br>Gly        | 427  |
| aa tcc<br>ys Ser          | att<br>Ile        | aat<br>Asn<br>75  | atg<br>Met        | caa<br>Gln        | gaa<br>Glu        | caa<br>Gln        | ata<br>Ile<br>80  | att<br>Ile        | gat<br>Asp        | gga<br>Gly        | tgg<br>Trp        | ttt<br>Phe<br>85  | tta<br>Leu        | gct<br>Ala        | 475  |
| ga ttt<br>rg Phe          | tgg<br>Trp<br>90  | ata<br>Ile        | ttt<br>Phe        | aag<br>Lys        | gat<br>Asp        | caa<br>Gln<br>95  | aat<br>Asn        | aat<br>Asn        | agt<br>Ser        | cac<br>His        | caa<br>Gln<br>100 | aca<br>Thr        | aat<br>Asn        | aga<br>Arg        | 523  |
| tt att<br>he Ile<br>105   | tca<br>Ser        | tgg<br>Trp        | ttt<br>Phe        | aag<br>Lys        | gat<br>Asp<br>110 | aat<br>Asn        | ttg<br>Leu        | gct<br>Ala        | agc<br>Ser        | cca<br>Pro<br>115 | gga<br>Gly        | ggg<br>Gly        | tat<br>Tyr        | gat<br>Asp        | 571  |
| gt atc<br>er Ile<br>20    | gct<br>Ala        | gaa<br>Glu        | cag<br>Gln        | atg<br>Met<br>125 | ggc<br>Gly        | cta<br>Leu        | aaa<br>Lys        | gta<br>Val        | gca<br>Ala<br>130 | gca<br>Ala        | tta<br>Leu        | aat<br>Asn        | gat<br>Asp        | atg<br>Met<br>135 | 619  |
| at ata<br>sp Ile          | tca<br>Ser        | aat<br>Asn        | gta<br>Val<br>140 | aat<br>Asn        | tat<br>Tyr        | act<br>Thr        | tct<br>Ser        | aag<br>Lys<br>145 | aca<br>Thr        | ggg<br>Gly        | gat<br>Asp        | act<br>Thr        | ata<br>Ile<br>150 | tat<br>Tyr        | 667  |
| at ggt<br>sn Gly          | gtt<br>Val        | tca<br>Ser<br>155 | gaa<br>Glu        | tta<br>Leu        | aaa<br>Lys        | aat<br>Asn        | atc<br>Ile<br>160 | aca<br>Thr        | gga<br>Gly        | aca<br>Thr        | act<br>Thr        | caa<br>Gln<br>165 | Lys               | atg<br>Met        | 715  |
| aa aca<br>ys Thr          | gat<br>Asp<br>170 | agt<br>Ser        | ttt<br>Phe        | caa<br>Gln        | aga<br>Arg        | gat<br>Asp<br>175 | tat<br>Tyr        | aca<br>Thr        | aaa<br>Lys        | tcc<br>Ser        | cag<br>Gln<br>180 | ser               | act<br>Thr        | tca<br>Ser        | 763  |
| tc acc<br>le Thr<br>185   | aat<br>Asn        | gga<br>Gly        | tta<br>Leu        | caa<br>Gln        | tta<br>Leu<br>190 | gga<br>Gly        | ttt<br>Phe        | aaa<br>Lys        | gtt<br>Val        | tca<br>Ser<br>195 | gct<br>Ala        | aaa<br>Lys        | gga<br>Gly        | ata<br>Ile        | 811  |
| tg gcc<br>al Ala<br>200   | tta<br>Leu        | gcc<br>Ala        | ggt<br>Gly        | gcg<br>Ala<br>205 | gat<br>Asp        | ttt<br>Phe        | gaa<br>Glu        | gca<br>Ala        | agt<br>Ser<br>210 | ۷a٦               | aac<br>Asn        | tat<br>Tyr        | aat<br>Asn        | tta<br>Leu<br>215 | 859  |
| cc act<br>er Thr          | acc<br>Thr        | gca<br>Ala        | act<br>Thr<br>220 | Glu               | acc<br>Thr        | aat<br>Asn        | aca<br>Thr        | ata<br>Ile<br>225 | tct<br>Ser        | gat<br>Asp        | aaa<br>Lys        | ttt<br>Phe        | acc<br>Thr<br>230 | ٧al               | 907  |
| ct tca<br>Pro Ser         | caa<br>Gln        | gaa<br>Glu<br>235 | gtc<br>Val        | aca<br>Thr        | tta<br>Leu        | gcg<br>Ala        | cca<br>Pro<br>240 | Gly               | cat<br>His        | aag<br>Lys        | gcg<br>Ala        | atc<br>Ile<br>245 | : Val             | aaa<br>Lys        | 955  |
| at agt<br>His Ser         | ttg<br>Leu<br>250 | Lys               | aaa<br>Lys        | atg<br>Met        | gta<br>Val        | tac<br>Tyr<br>255 | Ser               | gga<br>Gly        | acg<br>Thr        | cat<br>His        | gat<br>Asp<br>260 | Leu               | aaa<br>Lys        | gga<br>Gly        | 1003 |
| at tta<br>Asp Leu<br>265  | Thr               | att               | act<br>Thr        | ttt<br>Phe        | aat<br>Asn<br>270 | Asp               | aag<br>Lys        | gat<br>Asp        | tta<br>Leu        | gtt<br>Val<br>275 | Gln               | aaa<br>Lys        | ttt<br>Phe        | att<br>Ile        | 1051 |
| tat cca<br>Tyr Pro<br>280 | aat<br>Asn        | tat<br>Tyr        | aaa<br>Lys        | gct<br>Ala<br>285 | Ile               | gat<br>Asp        | tta<br>Leu        | tct<br>Ser        | aat<br>Asn<br>290 | ıle               | cgt<br>Arg        | aaa<br>Lys        | gca<br>Ala        | atg<br>Met<br>295 | 1099 |
| aca gaa<br>Thr Glu        | att               | gat<br>Asp        | gaa<br>Glu        | tgg               | aat<br>Asn        | cat<br>His        | gta<br>Val        | aaa<br>Lys        | cct               | acc               | gat<br>Asc        | ttc<br>Phe        | tat               | caa<br>Gln        | 1147 |

Page 14

| 38-21(52806) Sequence Listing_PCT_2.ST25.txt<br>300 305 310   |      |
|---|------|
| tta gtt ggg aat aaa aat tat ata aaa aac ggg gac act tta tac atc<br>Leu Val Gly Asn Lys Asn Tyr Ile Lys Asn Gly Asp Thr Leu Tyr Ile<br>315 320 325 | 1195 |
| gaa aca cct gct aaa ttc act ttg aat gga ggc aac cct tat tat aca<br>Glu Thr Pro Ala Lys Phe Thr Leu Asn Gly Gly Asn Pro Tyr Tyr Thr<br>330 335 340 | 1243 |
| gca acc ttt acg gaa tat gat gaa aat gga aat caa gtc aaa aca aag<br>Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Gln Val Lys Thr Lys<br>345 350 355 | 1291 |
| cgt tta aat aac aaa taagttactt aaaggtaatt cattaacaat gtatccatta<br>Arg Leu Asn Asn Lys<br>360   | 1346 |
| tataattaat ttataaaaat aatgttttaa aa   | 1378 |
| <210> 10  |      |
| <211> 364   |      |
| <212> PRT   |      |
| <213> Bacillus thuringiensis  |      |
| <400> 10  |      |
| Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu<br>1 5 10 15  |      |
| Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu<br>20 25 30   |      |
| Thr Thr Ser Ser His Ala Val Thr Asn Gln Gln Thr Ile Thr Gln Arg<br>35 40 45   |      |
| Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Gln Arg Asp<br>50 55 60   |      |
| Ile Glu Ser Lys Met Thr Gly Lys Ser Ile Asn Met Gln Glu Gln Ile 65 70 75 80   |      |
| Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn<br>85 90 95   |      |
| Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu<br>100 105 110  |      |
| Ala Ser Pro Gly Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys<br>115 120 125  |      |
| Page 15   |      |

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt Val Ala Ala Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser 130 140 Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile 145 150 155 160 Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr 165 170 175 Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe 180 185 190 Lys Val Ser Ala Lys Gly Ile Val Ala Leu Ala Gly Ala Asp Phe Glu 195 200 205 Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Thr 210 220 Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro 225 230 235 240 Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser 245 250 255 Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys 260 265 270Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu 275 280 285 Ser Asn Ile Arg Lys Ala Met Thr Glu Ile Asp Glu Trp Asn His Val 290 295 300 Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys 305 310 315 Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn 325 330 335 Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Asn 340 345 Gly Asn Gln Val Lys Thr Lys Arg Leu Asn Asn Lys 355 <210> 11.

Page 16

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> probe sequence, or amplification primer sequence for use with primer as set forth in SEQ ID NO 12, corresponding to CDS as set for th in SEQ ID NO 3 from 438-458, biased toward codons preferred in Bacillus species genes containing A or T in 3rd position

<400> 11 aataataatc atcaaacwaa t

21

<210> 12

<211> 21.

<212> DNA

<213> Artificial Sequence

<220>

<223> probe sequence, or amplification primer sequence for use with SEQ ID NO 11 corresponding to SEQ ID NO 3 from nucleotide position 9 78- 998, biased toward codons preferred in Bacillus species genes in which A or T is in 3rd position

<400> 12 attwggataw ataaattttt g

21

<210> 13

<211> 1101

<212> DNA

<213> Artificial Sequence

<220>

<223> coding sequence preferred for use in monocot species encoding a B
t TIC901 amino acid sequence variant

<220>

<221> CDS

<222> (1)..(1101)

<223>

# 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

| Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu 15  atg gtt tct acg ttc gcg tcc agc tcg atg tcc gcg ttc gca gcg gag Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu 20  gcc aaa agt cct gac ttg aac gtg tcc caa cag gtc ata ggc cct tac Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr 40  gca gaa tct tac atc gac atc gtc cag gac aga atg aag cag aga gac Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp 55  aaa gga tcc aaa ctc act ggc aaa ccc atc aac atg caa gag cag atc Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile 80  atc gat ggg tgg ttt ctc gca cga ttc tgg att ttc aag gat cag acc 28  aat aac cac cag aca aac agg ttc atc tca tgg ttt aag gat cag acc Asn Asn Ash His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile 100  gcc tca tct aag gga tac aac tca at g gcc gac aga cag atg ggc ctc aaa Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys 115  atc gaa gca gag aat gat atg gac gtg aca aat at gac gac tac gag cac ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys 115  atc gaa gca gag aat gat atg gac gtg aca aat at gcc gac tac act agt 116 Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 130  acc aaa cc gga gac aca at cac cac acc gcc att tcg gaa ctt aaa acc tac at gt 116 Glu Ala Glu Asn Asp Met Asp Val Thr Asp Ile Asp Tyr Thr Ser 130  aag acc gga gac acc acc at tac aac ggc att tcg gaa ctt aaa aac tat Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 145  aca aaa tcc gga cac aa at ga aag acc gat acc tca aag ggc ttc tcc gtg acc acc acc acc acc acc acc acc acc ac  | <400       | )> 1       | L3                |            |                 |            |            |                   |            |            |            | •          |            |            |            |            |   |     |
|--|------------|------------|-------------------|------------|-----------------|------------|------------|-------------------|------------|------------|------------|------------|------------|------------|------------|------------|---|-----|
| Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu 20  gcc aaa agt cct gac ttg aac gtg tcc caa cag gtc ata ggc cct tac Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr 45  gca gaa tct tac atc gac atc gtc cag gac aga atg aag cag aga gac Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp 50  aaa gga tcc aaa ctc act ggc aaa ccc atc acc atg caa gag cag atc Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile 70  atc gat ggg tgg ttt ctc gca cga ttc tgg att ttc aag gat cag aac Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn 95  aat aac cac cag aca aac agg ttc atc cat tgg ttt aag gat aac atc 100  gcc tca tct aag gga tac aac tca ata gcc gaa cag atg ggc ctc aaa Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys 115  atc gaa gca gag aat gat atg gac gtg aca aat atc gac gag gac cac atc act atg Ile Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 136  aag acc gga gac acc atc tac acc ggc atc acc at at a gcc gaa cag atg ggc ctc aac Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 116  acc gac gac gac acc cag aaa atg aag acc gat tcg acc at at acc act act atg Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 116  acc ggc acc cag aaa atg aag acc gac acc gac acc cag aaa acc acc   | Met        | aag<br>Lys | aac<br>Asn        | cgc<br>Arg | ttc<br>Phe<br>5 | agc<br>Ser | aag<br>Lys | gtc<br>Val        | gcc<br>Ala | Leu        | tgc<br>Cys | acg<br>Thr | gtg<br>Val | cct<br>Pro | Ile        | ctc<br>Leu |   | 48  |
| Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr 45 40 40 40 41 Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp 50 50 55 55 60 Ser Lys Leu Thr Gly Lys Pro Ile Asp Met Lys Gln Arg Asp 60 55 60 55 60 Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile 65 70 70 70 70 70 70 70 70 70 70 70 70 70   | atg<br>Met | gtt<br>Val | tct<br>Ser        | Thr        | ttc<br>Phe      | gcg<br>Ala | tcc<br>Ser | agc<br>Ser        | Ser        | atg<br>Met | tcc<br>Ser | gcg<br>Ala | ttc<br>Phe | Āla        | gcg<br>Ala | gag<br>Glu |   | 96  |
| Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  aaa gga tcc aaa ctc act ggc aaa ccc atc aac atg caa gag cag atc Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile 65  atc gat ggg tgg ttt ctc gca cga ttc tgg att ttc aag gat cag aac Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn 85  aat aac cac cag aca aac agg ttc atc tca tgg ttt aag gat aac atc Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile 100  gcc tca tct aag gga tac aac tca ata gcc gaa cag atg ggc ctc aaa Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys 115  atc gaa gca gag aat gat atg Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 130  aag acc gga gac aca atc tac aac ggc att tcg Ide Asp Tyr Thr Ser 145  acg ggc agc agc acc cag aaa atg aag acc ggc att tcg Thr Gly Asp Thr Ile 157  aca aaa tcc gag agc acc cag aaa atg aag acc gat agc ttc aaa aac tat 185  acg ggc agc agc acc cag aaa atg aag acc gat agc ttc caa agg gac tac Thr Gly Ser Thr Gln Lys Met Lys Thr Asn Gly Leu Gln Leu Gly Phe 180  acg ggc gca gca gca cac tcc gtg acc Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180  act tcg gtg acc tac aat ctg tct aca act acg act gag acc gac tcc gag 195  act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac acc Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Thr Glu Thr Asn Thr 210  act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac acc Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Thr Thr Asn Thr 210  act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Thr Thr Asn Thr 210  act tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc ccc cca Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Thr Thr Asn Thr 220  act tcc gac aag ttt acg gtt ccg tcc tcag gag gtt acg ttc ccc tca | gcc<br>Ala | aaa<br>Lys | Ser               | cct<br>Pro | gac<br>Asp      | ttg<br>Leu | aac<br>Asn | ٧a٦               | tcc<br>Ser | caa<br>Gln | cag<br>Gln | gtc<br>val | Ile        | ggc<br>Gly | cct<br>Pro | tac<br>Tyr | 1 | .44 |
| atc gat ggg tgg ttt ctc gca cga ttc tgg att ttc aag gat cag aac aca cac cag aca aca aca aca agg ttc atc file Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn 95  aat aac cac cag aca aca aca agg ttc atc tca tgg ttt aag gat aac atc Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile 100  gcc tca tct aag gga tac aac tca ata gcc gaa cag atg ggc ctc aaa Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys 115  atc gaa gca gag aat gat atg gac gtg aca aat atc gac tac act agt Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 130  aag acc gga gac aca act act aca ac ggc att tcg gaa ctt aaa aac tat Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 145  aca ggc agc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac Thr Gly Ser Thr Gln Lys Met Lys Thr Asn Gly Leu Gln Arg Asp Tyr 175  aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag cag ggc ttc Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180  aag gtg gca gca gca aca ggc tcg gtc gtc gtt ta gcc ggc gca gac ttc gag Lys Val Ala Ala Lys Gly Val Ala Ala Leu Ala Gly Ala Asp Phe Glu 205  act tcg gtg acc tac aat ctg tct aca act acc acc acc acc acc acc acc  | gca<br>Ala | Glu        | tct<br>Ser        | tac<br>Tyr | atc<br>Ile      | gac<br>Asp | I]e        | gtc<br>Val        | cag<br>Gln | gac<br>Asp | aga<br>Arg | Met        | aag<br>Lys | cag<br>Gln | aga<br>Arg | gac<br>Asp | 1 | .92 |
| aat aac cac cag aca aca agg ttc atc tca tgg ttt aag gat aac atc 100 lb ser Trp Phe Lys Asp Asn Ile 100 lb ser Trp Phe Lys Asp Asn Ile 100 lb ser Trp Phe Lys Asp Asn Ile 110 lb ser Trp Phe Lys Asp Asn Ile 110 lb ser Trp Phe Lys Asp Asn Ile 110 lb ser Trp Phe Lys Asp Asn Ile 110 lb ser Trp Phe Lys Asp Asn Ile 110 lb ser Trp Phe Lys Asp Asn Ile 110 lb ser Ile Ser Trp Phe Lys Asp Asn Ile 110 lb ser Ile Ser Trp Phe Lys Asp Asp Ile 110 lb ser Ile Ser Ile Ala Glu Gln Met Gly Leu Lys 115 lb ser Ile Ala Glu Gln Met Gly Leu Lys 112 lb ser Ile Ala Glu Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 130 lb ser Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Ile 150 lb ser Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 165 lb ser Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr 175 lb ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gly Phe 180 lb ser Thr Ser Val Thr Asn Gly Leu Gly Phe 180 lb ser Thr Ser Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 200 lb ser Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr 210 lb ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro   | Lys        | gga<br>Gly | tcc<br>Ser        | aaa<br>Lys | ctc<br>Leu      | Thr        | ggc<br>Gly | aaa<br>Lys        | ccc<br>Pro | atc<br>Ile | Asn        | atg<br>Met | caa<br>Gln | gag<br>Glu | cag<br>Gln | Ile        | 2 | 240 |
| Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile 100  gcc tca tct aag gga tac aac tca ata gcc gaa cag atg ggc ctc aaa Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys 125  atc gaa gca gag aat gat atg gac gtg aca aat atc gac tac act agt Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 130  aag acc gga gac aca atc tac aac ggc att tcg gaa ctt aaa aac tat Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 160  acg ggc agc acc caa aat atc Lys Thr Asp Ser Phe Gln Arg Asp Tyr 160  acg ggc agc acc caa aat Lys Thr Asp Ser Phe Gln Arg Asp Tyr Info Ser 175  aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180  aag gtg gca gca aca ggc gtc gtc gtc gtt tta gcc ggc gca gac ttc gag Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 205  act tcg gtg acc tac aat ctg tct aca act acg act gag acg aca aca Ct tcg Ite Ser Val Thr Tyr Asn Thr Thr Thr Thr Thr Thr Asn Thr 210  att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc ccc Cca Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro   | atc<br>Ile | gat<br>Asp | ggg<br>Gly        | tgg<br>Trp | Phe             | ctc<br>Leu | gca<br>Ala | cga<br>Arg        | ttc<br>Phe | Trp        | att<br>Ile | ttc<br>Phe | aag<br>Lys | gat<br>Asp | Gln        | aac<br>Asn | 2 | 288 |
| Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys 125  atc gaa gca gag aat gat atg gac gtg aca aat atc gac tac act agt Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 130  aag acc gga gac aca atc tac aac ggc att tcg gaa ctt aaa aac tat Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 145  acg ggc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr 175  aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180  aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 200  act tcg gtg acc tac aat ctg tct aca act acg act gag acg acc acc Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr 210  att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro   | aat<br>Asn | aac<br>Asn | cac<br>His        | Gln        | aca<br>Thr      | aac<br>Asn | agg<br>Arg | ttc<br>Phe        | Ile        | tca<br>Ser | tgg<br>Trp | ttt<br>Phe | aag<br>Lys | Asp        | aac<br>Asn | atc<br>Ile | 3 | 336 |
| aag acc gga gac aca atc tac aac ggc att tcg gaa ctt aaa aac tat Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 145  acg ggc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr 165  aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180  aag gtg gca gca aag ggc gtc gtc gtc gct tta gcc ggc gca gac ttc gag Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 200  act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr 210  att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro   | gcc<br>Ala | tca<br>Ser | Ser               | aag<br>Lys | gga<br>Gly      | tac<br>Tyr | aac<br>Asn | Ser               | ata<br>Ile | gcc<br>Ala | gaa<br>Glu | cag<br>Gln | Met        | ggc<br>Gly | ctc<br>Leu | aaa<br>Lys | 3 | 384 |
| Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 150  acg ggc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr 175  aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180  aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 200  act tcg gtg acc tac aat ctg tct aca act acg act gag acg aca aca Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr 210  att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca Tile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro  | atc<br>Ile | Glu        | gca<br>Ala        | gag<br>Glu | aat<br>Asn      | gat<br>Asp | Met        | gac<br>Asp        | gtg<br>Val | aca<br>Thr | aat<br>Asn | Ile        | gac<br>Asp | tac<br>Tyr | act<br>Thr | agt<br>Ser | 2 | 132 |
| Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr 175  aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180  aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 200  act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr 210  att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca 72 Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro   | Lys        | acc<br>Thr | gga<br>Gly        | gac<br>Asp | aca<br>Thr      | Ile        | Tyr        | aac<br>Asn        | ggc<br>Gly | att<br>Ile | Ser        | gaa<br>Glu | ctt<br>Leu | aaa<br>Lys | aac<br>Asn | Tyr        | 4 | 180 |
| Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180  aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 195  act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr 210  att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro   | acg<br>Thr | ggc<br>Gly | agc<br>Ser        | acc<br>Thr | Gln             | aaa<br>Lys | atg<br>Met | aag<br>Lys        | acc<br>Thr | Asp        | Ser        | ttt<br>Phe | caa<br>Gln | agg<br>Arg | Asp        | tac<br>Tyr |   | 528 |
| act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr 210  att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca Tle Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro   | aca<br>Thr | aaa<br>Lys | tcc<br>Ser        | Glu        | Ser             | acc<br>Thr | tcc<br>Ser | ٧a٦               | Thr        | Asn        | ggc<br>Gly | ctc<br>Leu | cag<br>Gln | Leu        | Gly        | ttc<br>Phe | ! | 576 |
| Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr 210  att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca  72  The Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr 220  att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca  72  The Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro  | aag<br>Lys | gtg<br>Val | gca<br>Ala<br>195 | gca<br>Ala | aag<br>Lys      | ggc<br>Gly | gtc<br>Val | gtc<br>Val<br>200 | gct<br>Ala | tta<br>Leu | gcc<br>Ala | ggc<br>Gly |            |            | ttc<br>Phe | gag<br>Glu | ( | 624 |
| ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro  | act<br>Thr | Ser        | ٧a١               | acc<br>Thr | tac<br>Tyr      | aat<br>Asn | Leu        | Ser               | aca<br>Thr | act<br>Thr | acg<br>Thr | Thr        | Glu        | acg<br>Thr | aac<br>Asn | aca<br>Thr | ( | 672 |
|  | Ile        | Ser        | gac<br>Asp        | aag<br>Lys | ttt<br>Phe      | Thr        | ' Val      | ccg<br>Pro        | tct<br>Ser | cag<br>Gln | Glu        | Val        | acg<br>Thr | ttc<br>Phe | cct<br>Pro | Pro        | ; | 720 |

|                   |                   |                   |                   |                   | 38-2              | 1(52              | 806)              | Seq               | uenc              | e Li              | stin              | g_PC              | т_2.              | ST25              | .txt              |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| ggc<br>Gly        | cac<br>His        | aag<br>Lys        | gca<br>Ala        | atc<br>Ile<br>245 | gtc<br>Val        | aag<br>Lys        | cac<br>His        | gac<br>Asp        | ctg<br>Leu<br>250 | agg<br>Arg        | aaa<br>Lys        | atg<br>Met        | gtc<br>Val        | tac<br>Tyr<br>255 | agc<br>Ser        | 768  |
| ggc<br>Gly        | acc<br>Thr        | cat<br>His        | gat<br>Asp<br>260 | ctc<br>Leu        | aaa<br>Lys        | ggc<br>Gly        | gac<br>Asp        | ctc<br>Leu<br>265 | atc<br>Ile        | gtg<br>Val        | tcg<br>Ser        | ttc<br>Phe        | aac<br>Asn<br>270 | gac<br>Asp        | aag<br>Lys        | 816  |
| gag<br>Glu        | ata<br>Ile        | gtc<br>Val<br>275 | cag<br>Gln        | aag<br>Lys        | ttc<br>Phe        | atc<br>Ile        | tac<br>Tyr<br>280 | cca<br>Pro        | aat<br>Asn        | tac<br>Tyr        | cgc<br>Arg        | gac<br>Asp<br>285 | atc<br>Ile        | aac<br>Asn        | ctc<br>Leu        | 864  |
| agt<br>Ser        | gac<br>Asp<br>290 | atc<br>Ile        | cga<br>Arg        | gag<br>Glu        | acc<br>Thr        | atg<br>Met<br>295 | atc<br>Ile        | gag<br>Glu        | atc<br>Ile        | gac<br>Asp        | gag<br>Glu<br>300 | tgg<br>Trp        | aac<br>Asn        | cac<br>His        | gtg<br>Val        | 912  |
| aac<br>Asn<br>305 | cct<br>Pro        | gtc<br>Val        | aat<br>Asn        | ttc<br>Phe        | tac<br>Tyr<br>310 | gaa<br>Glu        | ctc<br>Leu        | gta<br>Val        | gga<br>Gly        | gtt<br>Val<br>315 | aag<br>Lys        | aac<br>Asn        | cac<br>His        | atc<br>Ile        | aag<br>Lys<br>320 | 960  |
| aac<br>Asn        | ggt<br>Gly        | gaa<br>Glu        | aca<br>Thr        | ttg<br>Leu<br>325 | tac<br>Tyr        | atc<br>Ile        | gac<br>Asp        | acg<br>Thr        | ccg<br>Pro<br>330 | gct<br>Ala        | aag<br>Lys        | ttc<br>Phe        | atg<br>Met        | ttc<br>Phe<br>335 | aac<br>Asn        | 1008 |
| gga<br>Gly        | gcg<br>Ala        | aat<br>Asn        | cct<br>Pro<br>340 | Tyr               | tat<br>Tyr        | cga<br>Arg        | gct<br>Ala        | acc<br>Thr<br>345 | ttc<br>Phe        | acg<br>Thr        | gag<br>Glu        | tac<br>Tyr        | gat<br>Asp<br>350 | ggc<br>Gly        | aac<br>Asn        | 1056 |
| aac<br>Asn        | aat<br>Asn        | cct<br>Pro<br>355 | gtt<br>Val        | cag<br>Gln        | acc<br>Thr        | aag<br>Lys        | gtg<br>Val<br>360 | Leu               | agt<br>Ser        | gag<br>Glu        | aat<br>Asn        | ttc<br>Phe<br>365 | Lys               | ctg<br>Leu        |                   | 1101 |
| <b>-</b> 21       | ٥-                | 11                |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |

<210> 14

<211> 367

<212> PRT

<213> Artificial Sequence

<220>

<223> coding sequence preferred for use in monocot species encoding a B t TIC901 amino acid sequence variant

<400> 14

Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu 10 15

Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu 20 25 30

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr 35 40 45

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt
Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
50 55 60 Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile 65 70 75 80 Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn 85 90 95 Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile 100 105 110Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys 115 120 125 Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 130 135 140 Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 145 150 160 Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
165 170 175 Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180 185 190 Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 195 200 205 . Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr 210 215 220 Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro 225 230 235 240 Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser 245 250 255 Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys 260 265 270Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu 275 280 285 Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val 290 295 300

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys 305 310 315 320305 Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn 340 350 Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu 365 <210> 15 <211> 23 <212> DNA <213> Artificial Sequence <220> oligonucleotide primer coupled with prJPW152 SEQ ID NO 16 in ther mal amplification reactions <223> <400> 15 cctttggcag aaactttaac tcc 23 <210> 16 <211> 21 <212> DNA <213> Artificial Sequence <220> oligonucleotide primer coupled with prJPW151 SEQ ID NO 15 in ther mal amplification reactions <400> gtgtattctg gtacgcatga c 21 <210> 17 <211> 34 <212> DNA <213> Artificial Sequence

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<220> oligonucleotide primer coupled with prJPW183 SEQ ID NO 18 in ther mal amplification reactions <223> <400> 17 34 gccggatccc tagctgaata tgcagtagat aatg <210> 18 <211> 25 <212> DNA <213> Artificial Sequence <220> oligonucleotide primer coupled with prJPW186 SEQ ID NO 17 in ther mal amplification reactions <223> <400> 18 25 gtggcacgtt tataggccat tgttc <210> 19 <211> 23 <212> DNA <213> Artificial Sequence <220> oligonucleotide primer coupled with prJPW156 SEQ ID NO 20 in ther mal amplification reactions <223> <400> 19 23 cttttaggcc catctgttca gcg <210> 20 <211> 26 <212> DNA <213> Artificial Sequence <220>

<223> oligonucleotide primer coupled with prJPW155 SEQ ID NO 19 in ther
 mal amplification reactions

#### 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<400> 20 gccttagccg gtgcggattt tgaagc

26

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW170 SEQ ID NO 22 in ther
 mal amplification reactions

<400> 21

ggagcttatt tgttatttaa acgctttgtt ttgacttgat ttcc

44

<210> 22

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW168 SEQ ID NO 21 in ther
 mal amplification reactions

<400> 22

gccggatccc agtggatagg aatttgtttt cgtgctagg

39

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:24 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:SEQ ID NO:27-29 and template DNA homologo us to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 23 aayatgcarg arcarathat hgaygg

26

### 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 an d SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic9 01, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 24 aayatgcarg arcarathat hga

23

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 an d SEQ ID NO:24 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic9 01, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 25 aayatgcarg arcarathat

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer that, when used in a therm al amplification reaction with any of SEQ ID NO:27-29 and templat e DNA homologous to tic901, 1201, 407, 417, 431 and the like result in amplicon of from about 395 to about 425 base pairs

*:*:

```
38-21(52806) Sequence Listing_PCT_2.ST25.txt
<220>
<221> misc_feature
<222>
      (3)..(3)
<223> inosine
<220>
<221> misc_feature
<222> (9)..(9)
<223> inosine
<400> 26
                                                                     20
ggngayacna thtayaaygg
<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
       universal reverse amplification primer similar to SEQ ID NO:28 an
<223>
       d SEQ ID NO:29
<220>
<221> misc_feature
<222> (6)..(6)
<223> inosine
<220>
<221> misc_feature
<222> (24)..(24)
<223> inosine
<400> 27
tarttnggrt adatraaytt ytgnac
                                                                     26
```

```
38-21(52806) Sequence Listing_PCT_2.ST25.txt
<210>
      28
<211>
      23
<212> DNA
<213> Artificial Sequence
<220>
      universal reverse amplification primer similar to SEQ ID NO:27 an
      d SEQ ID NO:29
<220>
<221> misc_feature
<222> (6)..(6)
<223> inosine
<400> 28
tarttnggrt adatraaytt ytg
                                                                      23
<210> 29
<211>
      20
<212> DNA
<213> Artificial Sequence
<220>
<223>
       universal reverse amplification primer similar to SEQ ID NO:27 an
       d SEQ ID NO:28
<220>
<221>
       misc_feature
<222>
      (18)..(18)
<223>
       inosine
<400> 29
ggrtadatra ayttytgnac
                                                                      20
<210> 30
<211> 570
<212> DNA
```

# 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)..(570)

<223>

|                         |                    |                   |                   |                   | ٠.                |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |   |    |
|-------------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---|----|
| <400<br>ttt<br>Phe<br>1 | )> 3<br>tta<br>Leu | 0<br>gct<br>Ala   | aga<br>Arg        | ttt<br>Phe        | tgg<br>Trp        | ata<br>Ile        | ttt<br>Phe        | gag<br>Glu        | gat<br>Asp<br>10  | caa<br>Gln        | aat<br>Asn        | aat<br>Asn        | agt<br>Ser        | cac<br>His<br>15  | caa<br>Gln        | 4 | 48 |
| aca<br>Thr              | aat<br>Asn         | aga<br>Arg        | ttt<br>Phe<br>20  | att<br>Ile        | tca<br>Ser        | tgg<br>Trp        | ttt<br>Phe        | aag<br>Lys<br>25  | gat               | aat<br>Asn        | att<br>Ile        | gct<br>Ala        | agt<br>Ser<br>30  | tca               | aaa<br>Lys        | 9 | 96 |
| ggg<br>Gly              | tat<br>Tyr         | aat<br>Asn<br>35  | agt<br>Ser        | att<br>Ile        | gcg<br>Ala        | gag<br>Glu        | caa<br>Gln<br>40  | atg<br>Met        | ggt<br>Gly        | tta<br>Leu        | aaa<br>Lys        | ata<br>Ile<br>45  | gaa<br>Glu        | gca<br>Ala        | gaa<br>Glu        | 1 | 44 |
| aac<br>Asn              | gat<br>Asp<br>50   | atg<br>Met        | gat<br>Asp        | gta<br>Val        | aca<br>Thr        | aat<br>Asn<br>55  | ata<br>Ile        | gat<br>Asp        | tat<br>Tyr        | aca<br>Thr        | tct<br>Ser<br>60  | aag<br>Lys        | aca<br>Thr        | ggc<br>Gly        | gat<br>Asp        | 1 | 92 |
| acc<br>Thr<br>65        | att<br>Ile         | tat<br>Tyr        | aat<br>Asn        | ggt<br>Gly        | att<br>Ile<br>70  | tca<br>Ser        | gaa<br>Glu        | ttg<br>Leu        | aaa<br>Lys        | aat<br>Asn<br>75  | tat<br>Tyr        | aca<br>Thr        | gga<br>Gly        | tca<br>Ser        | act<br>Thr<br>80  | 2 | 40 |
| caa<br>Gln              | aag<br>Lys         | atg<br>Met        | aaa<br>Lys        | aca<br>Thr<br>85  | gat<br>Asp        | agt<br>Ser        | ttt<br>Phe        | caa<br>Gln        | aga<br>Arg<br>90  | gat<br>Asp        | tat<br>Tyr        | aca<br>Thr        | aaa<br>Lys        | tca<br>Ser<br>95  | gaa<br>Glu        | 2 | 88 |
| tct<br>Ser              | act<br>Thr         | tca<br>Ser        | gta<br>Val<br>100 | act<br>Thr        | aat<br>Asn        | gga<br>Gly        | tta<br>Leu        | caa<br>Gln<br>105 | tta<br>Leu        | gga<br>Gly        | ttt<br>Phe        | aaa<br>Lys        | gtt<br>Val<br>110 | gct<br>Ala        | gct<br>Ala        | 3 | 36 |
| aaa<br>Lys              | gga<br>Gly         | gta<br>Val<br>115 | gtt<br>Val        | gct<br>Ala        | ttg<br>Leu        | gct<br>Ala        | ggg<br>Gly<br>120 | gca<br>Ala        | gac<br>Asp        | ttt<br>Phe        | gaa<br>Glu        | acc<br>Thr<br>125 | agt<br>Ser        | gtt<br>Val        | act<br>Thr        | 3 | 84 |
| tat<br>Tyr              | aat<br>Asn<br>130  | cta<br>Leu        | tca<br>Ser        | act<br>Thr        | act<br>Thr        | aca<br>Thr<br>135 | act<br>Thr        | gaa<br>Glu        | aca<br>Thr        | aat<br>Asn        | aca<br>Thr<br>140 | ata<br>Ile        | tca<br>Ser        | gac<br>Asp        | aag<br>Lys        | 4 | 32 |
| ttt<br>Phe<br>145       | act<br>Thr         | gtc<br>Val        | cca<br>Pro        | tct<br>Ser        | caa<br>Gln<br>150 | gaa<br>Glu        | gtt<br>Val        | aca<br>Thr        | ttg<br>Leu        | cct<br>Pro<br>155 | cca<br>Pro        | gga<br>Gly        | cat<br>His        | aaa<br>Lys        | gcg<br>Ala<br>160 | 4 | 80 |
| ata<br>Ile              | gtg<br>Val         | aaa<br>Lys        | cat<br>His        | gat<br>Asp<br>165 | tta<br>Leu        | aga<br>Arg        | aaa<br>Lys        | atg<br>Met        | gtt<br>Val<br>170 | Tyr               | tct<br>Ser        | ggt<br>Gly        | act<br>Thr        | cat<br>His<br>175 | gat<br>Asp        | 5 | 28 |
| cta<br>Leu              | aag<br>Lys         | ggt<br>Gly        | gat<br>Asp<br>180 | Leu               | att<br>Ile        | gtg<br>Val        | agt<br>Ser        | ttt<br>Phe<br>185 | aat<br>Asn        | gat<br>Asp        | aaa<br>Lys        | gag<br>Glu        | att<br>Ile<br>190 |                   |                   | 5 | 70 |
|                         |                    |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |   |    |

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<210> 31

<211> 190

<212> PRT

<213> Bacillus thuringiensis

<400> 31

Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln 10 15

Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys 20 25 30

Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu 35 40 45

Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp 50 60

Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr 65 70 75 80

Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu 85 90 95

Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala 100 105 110

Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr 115 120 125

Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys
130 140

Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala 145 150 155 160

Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp 165 170 175

Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile 180 185 190

<210> 32

# 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<211> 1095 <212> DNA <213> Bacillus thuringiensis <220> <221> CDS <222> (1)..(1092)sequence encoding TIC431 precursor amino acid sequence <400> 32 atg aaa tac aag tct tca aaa gta gca atg tgt aca tta tcg gct tta Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu 48 atg ctt tcg aca atc gcc act cca agt ata tct gtt ttc gct gct gaa Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu 20 25 30 96 aca act gca tca cat aag gtt act aat cag caa aca att gca cag cgt Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg  $\frac{35}{40}$ 144 gca gaa tct tat atc gat att gtg cat aat aga atg aaa aaa cga gat Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp 50 60192 att gaa tca aaa atg aca ggt aaa cct att aat atg caa gaa caa ata 240 Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile att gat gga tgg ttt tta gct aga ttt tgg ata ttc aag gac caa aat Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn 288 90 aat agt cac caa aca aat aga ttt att tca tgg ttt aaa gat aat tta 336 Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu gct agt cca gga ggg tat aat agt atc gct aaa caa atg ggg tta aaa Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys 115 120 125 384 ata gaa gta tta aat gat atg gat ata tca aat gta aat tat act tct Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser 432 aag aca ggg gat act ata tat aat ggt gtt tcc gaa tta aaa aat atc Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile 480 150 aca ggt aca act caa aaa atg aaa aca gat agt ttt caa aga gat tat Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr 165 170 175528

|   | 38-21(52806) s                              | Sequence Listing_PC                             | T_2.ST25.txt                           |
|---|---|---|--|
| aca aaa tca cag tca<br>Thr Lys Ser Gln Ser<br>180             | a act tca atc ac<br>Thr Ser Ile Th<br>18    | cc aat gga tta caa<br>nr Asn Gly Leu Gln<br>35  | tta gga ttt 576<br>Leu Gly Phe<br>190  |
| aaa gtt tct gcc aaa<br>Lys Val Ser Ala Lys<br>195             | a ggg gtg ata go<br>s Gly Val Ile Al<br>200 | ct tta gca gga gca<br>la Leu Ala Gly Ala<br>205 | gac ttc gaa 624<br>Asp Phe Glu         |
| gca agt gtc aac ta<br>Ala ser Val Asn Ty<br>210               | t aat tta tcc ac<br>r Asn Leu Ser Th<br>215 | ct acc gca act gaa<br>nr Thr Ala Thr Glu<br>220 | acc aat ata 672<br>Thr Asn Ile         |
| ata tct gat aaa tt <sup>.</sup><br>Ile Ser Asp Lys Pho<br>225 | t acc gtt cct to<br>E Thr Val Pro Se<br>230 | ca caa gaa gtt aca<br>er Gln Glu Val Thr<br>235 | tta gcg cca 720<br>Leu Ala Pro<br>240  |
| gga cat aag gcg ato<br>Gly His Lys Ala Ilo<br>24              | e Val Lys His Se                            | gt tta aag aaa atg<br>er Leu Lys Lys Met<br>250 | gta tac tcc 768<br>Val Tyr Ser<br>255  |
| gga acg cat gat tta<br>Gly Thr His Asp Le<br>260              | I LYS GIY ASP LE                            | ta aca att act ttt<br>eu Thr Ile Thr Phe<br>65  | aat gat aag 816<br>Asn Asp Lys<br>270  |
| gat tta gtt caa aa<br>Asp Leu Val Gln Ly:<br>275              | a ttt att tat co<br>s Phe Ile Tyr Pr<br>280 | ca aat tat aaa gct<br>ro Asn Tyr Lys Ala<br>285 | att gat tta 864<br>Ile Asp Leu         |
| tct aat att cgt aa<br>Ser Asn Ile Arg Ly<br>290               | a gca ctg act ga<br>s Ala Leu Thr Gl<br>295 | aa att gat gaa tgg<br>lu Ile Asp Glu Trp<br>300 | aat cat gta 912<br>Asn His Val         |
| aaa cct acc gat tt<br>Lys Pro Thr Asp Ph<br>305               | c tat caa tta gt<br>e Tyr Gln Leu Va<br>310 | tt ggg aac aaa aat<br>al Gly Asn Lys Asn<br>315 | tat ata aaa 960<br>Tyr Ile Lys<br>320  |
| aac ggg gac act tt<br>Asn Gly Asp Thr Le<br>32                | u Tyr Ile Glu Th                            | ca cct gct aaa ttc<br>hr Pro Ala Lys Phe<br>330 | act ttg aat 1008<br>Thr Leu Asn<br>335 |
| gga gga aac cct ta<br>Gly Gly Asn Pro Ty<br>340               | t tat aca gca ac<br>r Tyr Thr Ala Th<br>34  | cc ttt acg gaa tat<br>hr Phe Thr Glu Tyr<br>45  | gat gaa agt 1056<br>Asp Glu Ser<br>350 |
| gga aat caa gtc aa<br>Gly Asn Gln Val Ly:<br>355              | a aca aag cat tt<br>s Thr Lys His Le<br>360 | ta agt gtc aaa taa<br>eu Ser Val Lys            | 1095                                   |
| <210> 33  |   |   |  |
| ~211\ 36 <i>1</i>   |   |   |  |

<211> 364

<212> PRT

<213> Bacillus thuringiensis

<400> 33

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu Page 30

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt 10 15 Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu 20 25 30 Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg
35 40 45 Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp 50 55 60 Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile 65 70 75 80 Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn 85 90 95 Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu 100 105 110Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys 115 120 125 Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser 130 135 140 Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile 145 150 155 160 Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
165 170 175 Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe 180 185 190 Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu 195 200 205 Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile 210 215 220 Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro 225 230 235 240 Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser 245 250 255

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys 260 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu 275 280 285

Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val 290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys 305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn 325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser 340 345

Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys 355